

FEB 2 8 2003

Query= SEQ ID NO:1 (426 letters)

Score E (bits) Value

Sequences producing significant alignments:

AC024580.6.1.193609

<u>299</u> 7e-79

>AC024580.6.1.193609 Length = 193609

Score = 299 bits (151), Expect = 7e-79
Identities = 151/151 (100%)
Strand = Plus / Plus

Query: 280 aaaccagagattggaggtaaagccaggaaacacagaagagagacaccgacaggagaggg 339

Query: 340 gaacaaggaagtggcaggcagagcttagagg 370

Sbjct: 178606 gaacaaggaagtggcaggcagagcttagagg 178636

Score = 174 bits (88), Expect = 3e-41 Identities = 88/88 (100%)

Strand = Plus / Plus

Query: 1 atggctcctccctccgtcccctggtcctcctcgtcctcttgctgagcctggcagag 60

Sbjct: 172458 atggctcctcctcctcctcctcctcctcctcctcctcgtcctcttgctgagcctggcagag 172517

Query: 61 actccagcatccgcacctgcccaccggg 88

Sbjct: 172518 actccagcatccgcacctgcccaccggg 172545

Score = 163 bits (82), Expect = 1e-37
Identities = 82/82 (100%)
Strand = Plus / Plus

Query: 136 gtcctccaccttccccaaatgggtgaccaagacggaaagagggagacagcccttgagatc 195

Sbjct: 177520 gtcctccaccttccccaaatgggtgaccaagacggaaagagggagacagcccttgagatc 177579

Query: 196 ctagacctgtggaaggccatcg 217

Sbjct: 177580 ctagacctgtggaaggccatcg 177601

Score = 113 bits (57), Expect = 9e-23
Identities = 57/57 (100%)

Strand = Plus / Plus

Query: 370 gatctgggcatgctcagcatgaaaattcccaaggaggaagatgtcctgaagtcatag 426

Sbjct: 180563 gatctgggcatgctcagcatgaaaattcccaaggaggaagatgtcctgaagtcatag 180619

Score = 99.6 bits (50), Expect = 1e-18

Identities = 50/50 (100%)

Strand = Plus / Plus

Query: 87 gggacgaggaggctggacctcaatagtgctggctaccttctgggtcccg 136

Sbjct: 175934 gggacgaggaggctggaccctcaatagtgctggctaccttctgggtcccg 175983